

RECEIVED
JAN 16 2004
TECH CENTER 1600/2900



OIIPE

ENTERED

RAW SEQUENCE LISTING

DATE: 06/06/2003

PATENT APPLICATION: US/10/045,400C

TIME: 08:03:09

Input Set : A:\P-CAN 1004 Sequence Listing.txt

Output Set: N:\CRF4\06062003\J045400C.raw

3 <110> APPLICANT: Moon, Chulso
4 Mao, Li
6 <120> TITLE OF INVENTION: DAP-Kinase and HOXA9, Two Human Genes Associated with
Genesis,
7 Progression, and Aggressiveness of Non-Small Cell Lung Cancer
9 <130> FILE REFERENCE: 10620-1U1
11 <140> CURRENT APPLICATION NUMBER: 10/045,400C
12 <141> CURRENT FILING DATE: 2001-11-29
14 <150> PRIOR APPLICATION NUMBER: US 60/250,083
15 <151> PRIOR FILING DATE: 2000-11-29
17 <160> NUMBER OF SEQ ID NOS: 7
19 <170> SOFTWARE: PatentIn version 3.1
21 <210> SEQ ID NO: 1
22 <211> LENGTH: 20
23 <212> TYPE: DNA
24 <213> ORGANISM: Artificial
26 <220> FEATURE:
27 <223> OTHER INFORMATION: HoxA9 PCR Primer
29 <400> SEQUENCE: 1
30 ccggccttat ggcattaaac
33 <210> SEQ ID NO: 2
34 <211> LENGTH: 20
35 <212> TYPE: DNA
36 <213> ORGANISM: Artificial
38 <220> FEATURE:
39 <223> OTHER INFORMATION: HoxA9 PCR Primer
41 <400> SEQUENCE: 2
42 agttggctgc tgggttattg
45 <210> SEQ ID NO: 3
46 <211> LENGTH: 218
47 <212> TYPE: DNA
48 <213> ORGANISM: Artificial
50 <220> FEATURE:
51 <223> OTHER INFORMATION: HoxA9 Probe
53 <400> SEQUENCE: 3
54 ccggccttat ggcattaaac ctgaaccgct gtccggccaga aggggtgact gtccacgct 60
56 tgacactcac actttgtccc tgactgacta tgcttggtgt tctcctccag ttgatagaga 120
58 aaaacaaccc agcgaaggcg ccttctccga aaacaatgcc gagaatgaga gcggcggaga 180
60 caagcccccc atcgatccca ataaccagc agccaact 218
63 <210> SEQ ID NO: 4
64 <211> LENGTH: 5910
65 <212> TYPE: DNA
66 <213> ORGANISM: Homo sapiens
68 <220> FEATURE:

RECEIVED
JAN 29 2004
TECHNOLOGY CENTER R3700

RAW SEQUENCE LISTING

DATE: 06/06/2003

PATENT APPLICATION: US/10/045,400C

TIME: 08:03:09

Input Set : A:\P-CAN 1004 Sequence Listing.txt

Output Set: N:\CRF4\06062003\J045400C.raw

69 <221> NAME/KEY: CDS

70 <222> LOCATION: (337)..(4632)

71 <223> OTHER INFORMATION:

W--> 73 <400> 4

```

74 cggaggacag ccggaccgag ccaacgccgg ggactttgtt ccctccacgg aggggactcg      60
76 gcaactcgca gcggcagggt ctggggccgg cgcttgggag ggatctgcgc cccccactca      120
78 ctccctagct gtgttcccgc cgccgccccg gctagtctcc ggcgctggcg cctatggctg      180
80 gcctccgaca gcgctccgga gggaccgggg gagctcccag gcgcccggga ctggagactg      240
82 atgcatgagg ggcctacgga ggcgcaggag cggtggtgat ggtctgggaa gcggagctga      300
84 agtcccctgg gctttggtga ggcgtgacag tttatc atg acc gtg ttc agg cag      354
85                                     Met Thr Val Phe Arg Gln
86                                     1           5
88 gaa aac gtg gat gat tac tac gac acc ggc gag gaa ctt ggc agt gga      402
89 Glu Asn Val Asp Asp Tyr Tyr Asp Thr Gly Glu Glu Leu Gly Ser Gly
90                                     10          15          20
92 cag ttt gcg gtt gtg aag aaa tgc cgt gag aaa agt acc ggc ctc cag      450
93 Gln Phe Ala Val Val Lys Lys Cys Arg Glu Lys Ser Thr Gly Leu Gln
94                                     25          30          35
96 tat gcc gcc aaa ttc atc aag aaa agg agg act aag tcc agc cgg cgg      498
97 Tyr Ala Ala Lys Phe Ile Lys Lys Arg Arg Thr Lys Ser Ser Arg Arg
98                                     40          45          50
100 ggt gtg agc cgc gag gac atc gag cgg gag gtc agc atc ctg aag gag      546
101 Gly Val Ser Arg Glu Asp Ile Glu Arg Glu Val Ser Ile Leu Lys Glu
102 55                                     60          65          70
104 atc cag cac ccc aat gtc atc acc ctg cac gag gtc tat gag aac aag      594
105 Ile Gln His Pro Asn Val Ile Thr Leu His Glu Val Tyr Glu Asn Lys
106                                     75          80          85
108 acg gac gtc atc ctg atc ttg gaa ctc gtt gca ggt ggc gag ctg ttt      642
109 Thr Asp Val Ile Leu Ile Leu Glu Leu Val Ala Gly Gly Glu Leu Phe
110                                     90          95          100
112 gac ttc tta gct gaa aag gaa tct tta act gaa gag gaa gca act gaa      690
113 Asp Phe Leu Ala Glu Lys Glu Ser Leu Thr Glu Glu Glu Ala Thr Glu
114                                     105          110          115
116 ttt ctc aaa caa att ctt aat ggt gtt tac tac ctg cac tcc ctt caa      738
117 Phe Leu Lys Gln Ile Leu Asn Gly Val Tyr Tyr Leu His Ser Leu Gln
118                                     120          125          130
120 atc gcc cac ttt gat ctt aag cct gag aac ata atg ctt ttg gat aga      786
121 Ile Ala His Phe Asp Leu Lys Pro Glu Asn Ile Met Leu Leu Asp Arg
122 135                                     140          145          150
124 aat gtc ccc aaa cct cgg atc aag atc att gac ttt ggg ttg gcc cat      834
125 Asn Val Pro Lys Pro Arg Ile Lys Ile Ile Asp Phe Gly Leu Ala His
126                                     155          160          165
128 aaa att gac ttt gga aat gaa ttt aaa aac ata ttt ggg act cca gag      882
129 Lys Ile Asp Phe Gly Asn Glu Phe Lys Asn Ile Phe Gly Thr Pro Glu
130                                     170          175          180
132 ttt gtc gct cct gag ata gtc aac tat gaa cct ctt ggt ctt gag gca      930
133 Phe Val Ala Pro Glu Ile Val Asn Tyr Glu Pro Leu Gly Leu Glu Ala
134                                     185          190          195
136 gat atg tgg agt atc ggg gta ata acc tat atc ctc cta agt ggg gcc      978

```

RAW SEQUENCE LISTING

DATE: 06/06/2003

PATENT APPLICATION: US/10/045,400C

TIME: 08:03:09

Input Set : A:\P-CAN 1004 Sequence Listing.txt

Output Set: N:\CRF4\06062003\J045400C.raw

137	Asp	Met	Trp	Ser	Ile	Gly	Val	Ile	Thr	Tyr	Ile	Leu	Leu	Ser	Gly	Ala	
138		200					205					210					
140	tcc	cca	ttt	ctt	gga	gac	act	aag	caa	gaa	acg	tta	gca	aat	gta	tcc	1026
141	Ser	Pro	Phe	Leu	Gly	Asp	Thr	Lys	Gln	Glu	Thr	Leu	Ala	Asn	Val	Ser	
142	215					220					225					230	
144	gct	gtc	aac	tac	gaa	ttt	gag	gat	gaa	tac	ttc	agt	aat	acc	agt	gcc	1074
145	Ala	Val	Asn	Tyr	Glu	Phe	Glu	Asp	Glu	Tyr	Phe	Ser	Asn	Thr	Ser	Ala	
146					235					240					245		
148	cta	gcc	aaa	gat	ttc	ata	aga	aga	ctt	ctg	gtc	aag	gat	cca	aag	aag	1122
149	Leu	Ala	Lys	Asp	Phe	Ile	Arg	Arg	Leu	Leu	Val	Lys	Asp	Pro	Lys	Lys	
150				250					255					260			
152	aga	atg	aca	att	caa	gat	agt	ttg	cag	cat	ccc	tgg	atc	aag	cct	aaa	1170
153	Arg	Met	Thr	Ile	Gln	Asp	Ser	Leu	Gln	His	Pro	Trp	Ile	Lys	Pro	Lys	
154			265					270					275				
156	gat	aca	caa	cag	gca	ctt	agt	aga	aaa	gca	tca	gca	gta	aac	atg	gag	1218
157	Asp	Thr	Gln	Gln	Ala	Leu	Ser	Arg	Lys	Ala	Ser	Ala	Val	Asn	Met	Glu	
158		280						285					290				
160	aaa	ttc	aag	aag	ttt	gca	gcc	cgg	aaa	aaa	tgg	aaa	caa	tcc	gtt	cgc	1266
161	Lys	Phe	Lys	Lys	Phe	Ala	Ala	Arg	Lys	Lys	Trp	Lys	Gln	Ser	Val	Arg	
162	295					300					305					310	
164	ttg	ata	tca	ctg	tgc	caa	aga	tta	tcc	agg	tca	ttc	ctg	tcc	aga	agt	1314
165	Leu	Ile	Ser	Leu	Cys	Gln	Arg	Leu	Ser	Arg	Ser	Phe	Leu	Ser	Arg	Ser	
166					315					320					325		
168	aac	atg	agt	gtt	gcc	aga	agc	gat	gat	act	ctg	gat	gag	gaa	gac	tcc	1362
169	Asn	Met	Ser	Val	Ala	Arg	Ser	Asp	Asp	Thr	Leu	Asp	Glu	Glu	Asp	Ser	
170				330					335					340			
172	ttt	gtg	atg	aaa	gcc	atc	atc	cat	gcc	atc	aac	gat	gac	aat	gtc	cca	1410
173	Phe	Val	Met	Lys	Ala	Ile	Ile	His	Ala	Ile	Asn	Asp	Asp	Asn	Val	Pro	
174			345					350					355				
176	ggc	ctg	cag	cac	ctt	ctg	ggc	tca	tta	tcc	aac	tat	gat	gtt	aac	caa	1458
177	Gly	Leu	Gln	His	Leu	Leu	Gly	Ser	Leu	Ser	Asn	Tyr	Asp	Val	Asn	Gln	
178		360					365					370					
180	ccc	aac	aag	cac	ggg	aca	cct	cca	tta	ctc	att	gct	gct	ggc	tgt	ggg	1506
181	Pro	Asn	Lys	His	Gly	Thr	Pro	Pro	Leu	Leu	Ile	Ala	Ala	Gly	Cys	Gly	
182	375					380					385				390		
184	aat	att	caa	ata	cta	cag	ttg	ctc	att	aaa	aga	ggc	tcg	aga	atc	gat	1554
185	Asn	Ile	Gln	Ile	Leu	Gln	Leu	Leu	Ile	Lys	Arg	Gly	Ser	Arg	Ile	Asp	
186					395					400					405		
188	gtc	cag	gat	aag	ggc	ggg	tcc	aat	gcc	gtc	tac	tgg	gct	gct	cgg	cat	1602
189	Val	Gln	Asp	Lys	Gly	Gly	Ser	Asn	Ala	Val	Tyr	Trp	Ala	Ala	Arg	His	
190				410					415					420			
192	ggc	cac	gtc	gat	acc	ttg	aaa	ttt	ctc	agt	gag	aac	aaa	tgc	cct	ttg	1650
193	Gly	His	Val	Asp	Thr	Leu	Lys	Phe	Leu	Ser	Glu	Asn	Lys	Cys	Pro	Leu	
194			425					430					435				
196	gat	gtg	aaa	gac	aag	tct	gga	gag	atg	gcc	ctc	cac	gtg	gca	gct	cgc	1698
197	Asp	Val	Lys	Asp	Lys	Ser	Gly	Glu	Met	Ala	Leu	His	Val	Ala	Ala	Arg	
198		440					445					450					
200	tat	ggc	cat	gct	gac	gtg	gct	caa	gtt	act	tgt	gca	gct	tcg	gct	caa	1746
201	Tyr	Gly	His	Ala	Asp	Val	Ala	Gln	Val	Thr	Cys	Ala	Ala	Ser	Ala	Gln	

RAW SEQUENCE LISTING

DATE: 06/06/2003

PATENT APPLICATION: US/10/045,400C

TIME: 08:03:09

Input Set : A:\P-CAN 1004 Sequence Listing.txt

Output Set: N:\CRF4\06062003\J045400C.raw

202	455		460		465		470	
204	atc	cca	ata	tcc	agg	aca	aag	gaa
205	Ile	Pro	Ile	Ser	Arg	Thr	Lys	Glu
206				475				480
208	gct	tgg	cac	ggc	tat	tac	tct	gtg
209	Ala	Trp	His	Gly	Tyr	Tyr	Ser	Val
210				490				495
212	tgt	aac	gtg	aac	atc	aag	aac	cga
213	Cys	Asn	Val	Asn	Ile	Lys	Asn	Arg
214				505				510
216	gcc	tct	gcc	agg	ggc	tac	cac	gac
217	Ala	Ser	Ala	Arg	Gly	Tyr	His	Asp
218				520				525
220	gga	gcc	gac	ctt	aat	gct	tgc	gac
221	Gly	Ala	Asp	Leu	Asn	Ala	Cys	Asp
222	535							540
224	ctg	gct	gta	aga	cgg	tgt	cag	atg
225	Leu	Ala	Val	Arg	Arg	Cys	Gln	Met
226								555
228	caa	ggg	tgt	ttc	gtc	gat	tat	caa
229	Gln	Gly	Cys	Phe	Val	Asp	Tyr	Gln
230				570				575
232	cat	gtg	gca	tgt	aaa	gat	ggc	aac
233	His	Val	Ala	Cys	Lys	Asp	Gly	Asn
234				585				590
236	gaa	gca	aac	tgc	aat	ttg	gac	atc
237	Glu	Ala	Asn	Cys	Asn	Leu	Asp	Ile
238				600				605
240	ctg	cac	ctt	gcg	gcc	aac	aac	gga
241	Leu	His	Leu	Ala	Ala	Asn	Asn	Gly
242	615							620
244	tgt	ctg	atg	gga	gcc	agc	gtt	gag
245	Cys	Leu	Met	Gly	Ala	Ser	Val	Glu
246				635				640
248	gca	gaa	gat	ctt	gct	aga	tcg	gaa
249	Ala	Glu	Asp	Leu	Ala	Arg	Ser	Glu
250				650				655
252	ctt	gca	aga	ctt	cga	aag	gat	acg
253	Leu	Ala	Arg	Leu	Arg	Lys	Asp	Thr
254				665				670
256	ctc	cga	ccc	aca	cag	aac	ctg	cag
257	Leu	Arg	Pro	Thr	Gln	Asn	Leu	Gln
258				680				685
260	ggc	cac	tcg	gga	tcc	ggg	aaa	acc
261	Gly	His	Ser	Gly	Ser	Gly	Lys	Thr
262	695							700
264	ggg	ctg	ctg	agg	agc	ttt	ttc	aga
265	Gly	Leu	Leu	Arg	Ser	Phe	Phe	Arg
266								715

RAW SEQUENCE LISTING

DATE: 06/06/2003

PATENT APPLICATION: US/10/045,400C

TIME: 08:03:09

Input Set : A:\P-CAN 1004 Sequence Listing.txt

Output Set: N:\CRF4\06062003\J045400C.raw

268	acc	aac	tcc	agc	agg	ttc	cca	cct	tca	ccc	ctg	gct	tct	aag	ccc	aca	2562
269	Thr	Asn	Ser	Ser	Arg	Phe	Pro	Pro	Ser	Pro	Leu	Ala	Ser	Lys	Pro	Thr	
270				730					735					740			
272	gtc	tca	gtg	agc	atc	aac	aac	ctg	tac	cca	ggc	tgc	gag	aac	gtg	agt	2610
273	Val	Ser	Val	Ser	Ile	Asn	Asn	Leu	Tyr	Pro	Gly	Cys	Glu	Asn	Val	Ser	
274			745					750					755				
276	gtg	agg	agc	cgc	agc	atg	atg	ttc	gag	ccg	ggg	ctt	acc	aaa	ggg	atg	2658
277	Val	Arg	Ser	Arg	Ser	Met	Met	Phe	Glu	Pro	Gly	Leu	Thr	Lys	Gly	Met	
278		760					765					770					
280	ctg	gag	gtg	ttt	gtg	gcc	ccg	acc	cac	cac	ccg	cac	tgc	tcg	gcc	gat	2706
281	Leu	Glu	Val	Phe	Val	Ala	Pro	Thr	His	His	Pro	His	Cys	Ser	Ala	Asp	
282	775					780					785				790		
284	gac	cag	tcc	acc	aag	gcc	atc	gac	atc	cag	aac	gct	tat	ttg	aat	gga	2754
285	Asp	Gln	Ser	Thr	Lys	Ala	Ile	Asp	Ile	Gln	Asn	Ala	Tyr	Leu	Asn	Gly	
286				795						800					805		
288	gtt	ggc	gat	ttc	agc	gtg	tgg	gag	ttc	tct	gga	aat	cct	gtg	tat	ttc	2802
289	Val	Gly	Asp	Phe	Ser	Val	Trp	Glu	Phe	Ser	Gly	Asn	Pro	Val	Tyr	Phe	
290				810					815					820			
292	tgc	tgt	tat	gac	tat	ttt	gct	gca	aat	gat	ccc	acg	tca	atc	cat	gtt	2850
293	Cys	Cys	Tyr	Asp	Tyr	Phe	Ala	Ala	Asn	Asp	Pro	Thr	Ser	Ile	His	Val	
294			825					830					835				
296	gtt	gtc	ttt	agt	cta	gaa	gag	ccc	tat	gag	atc	cag	ctg	aac	cca	gtg	2898
297	Val	Val	Phe	Ser	Leu	Glu	Glu	Pro	Tyr	Glu	Ile	Gln	Leu	Asn	Pro	Val	
298		840					845					850					
300	att	ttc	tgg	ctc	agt	ttc	ctg	aag	tcc	ctt	gtc	cca	gtt	gaa	gaa	ccc	2946
301	Ile	Phe	Trp	Leu	Ser	Phe	Leu	Lys	Ser	Leu	Val	Pro	Val	Glu	Glu	Pro	
302	855					860					865				870		
304	ata	gcc	ttc	ggg	ggc	aag	ctg	aag	aac	cca	ctc	caa	gtt	gtc	ctg	gtg	2994
305	Ile	Ala	Phe	Gly	Gly	Lys	Leu	Lys	Asn	Pro	Leu	Gln	Val	Val	Leu	Val	
306				875					880					885			
308	gcc	acc	cac	gct	gac	atc	atg	aat	gtt	cct	cga	ccg	gct	gga	ggc	gag	3042
309	Ala	Thr	His	Ala	Asp	Ile	Met	Asn	Val	Pro	Arg	Pro	Ala	Gly	Gly	Glu	
310				890					895					900			
312	ttt	gga	tat	gac	aaa	gac	aca	tcg	ttg	ctg	aaa	gag	att	agg	aac	agg	3090
313	Phe	Gly	Tyr	Asp	Lys	Asp	Thr	Ser	Leu	Leu	Lys	Glu	Ile	Arg	Asn	Arg	
314			905					910					915				
316	ttt	gga	aat	gat	ctt	cac	att	tca	aat	aag	ctg	ttt	gtt	ctg	gat	gct	3138
317	Phe	Gly	Asn	Asp	Leu	His	Ile	Ser	Asn	Lys	Leu	Phe	Val	Leu	Asp	Ala	
318		920					925					930					
320	ggg	gct	tct	ggg	tca	aag	gac	atg	aag	gta	ctt	cga	aat	cat	ctg	caa	3186
321	Gly	Ala	Ser	Gly	Ser	Lys	Asp	Met	Lys	Val	Leu	Arg	Asn	His	Leu	Gln	
322	935				940					945					950		
324	gaa	ata	cga	agc	cag	att	gtt	tcg	gtc	tgt	cct	ccc	atg	act	cac	ctg	3234
325	Glu	Ile	Arg	Ser	Gln	Ile	Val	Ser	Val	Cys	Pro	Pro	Met	Thr	His	Leu	
326				955					960					965			
328	tgt	gag	aaa	atc	atc	tcc	acg	ctg	cct	tcc	tgg	agg	aag	ctc	aat	gga	3282
329	Cys	Glu	Lys	Ile	Ile	Ser	Thr	Leu	Pro	Ser	Trp	Arg	Lys	Leu	Asn	Gly	
330				970					975					980			
332	ccc	aac	cag	ctg	atg	tcg	ctg	cag	cag	ttt	gtg	tac	gac	gtg	cag	gac	3330

VERIFICATION SUMMARY

DATE: 06/06/2003

PATENT APPLICATION: US/10/045,400C

TIME: 08:03:10

Input Set : A:\P-CAN 1004 Sequence Listing.txt

Output Set: N:\CRF4\06062003\J045400C.raw

L:73 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:4,Line#:71

L:882 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:6,Line#:880